



5/AAA

SEQUENCE LISTING

<110> Glaxo Group Limited.

<120> Antibodies to CD23, derivatives thereof, and their therapeutic uses.

<130> PG3433

<140> CA 2,328,606

<141> 1999-05-07

<150> PCT/GB99/01434

<151> 1999-05-07

<150> GB 9809839.5

<151> 1998-05-09

<160> 53

<170> PatentIn Ver 2.1

<210> 1

<211> 415

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (3)..(413)

<400> 1

aa gct tta cag tta ctc agc aca cag gac ctc acc atg gat ttt ggg 47
Ala Leu Gln Leu Leu Ser Thr Gln Asp Leu Thr Met Asp Phe Gly
1 5 10 15

ctg att ttt ttt att gtt ctt tta aaa ggg gtc cag agt gaa gtg aag 95
Leu Ile Phe Phe Ile Val Leu Leu Lys Gly Val Gln Ser Glu Val Lys
20 25 30

ctt gag gag tct gga gga ggc ttg gtg caa cct gga gga tcc atg aaa 143
Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys
35 40 45

ctc tcc tgt gta gcc tct gga ttt act ttc agt ggc tac tgg atg tct 191
Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Gly Tyr Trp Met Ser
50 55 60

tgg gtc cgc cag tct cca gag aag ggg ctt gag tgg gtt gct gaa att 239
Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile
65 70 75

aga ttg aaa tct gat aat tat gca aca cat tat gcg gag tct gtg aaa 287
Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser Val Lys
80 85 90 95

ggg aag ttc acc atc tca aga gat gat tcc aaa agt cgt ctc tac ctg 335
Gly Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg Leu Tyr Leu
100 105 110

caa atg aac agc tta aga gct gaa gac agt gga gtt tat tac tgt aca 383
Gln Met Asn Ser Leu Arg Ala Glu Asp Ser Gly Val Tyr Tyr Cys Thr

115	120	125	
gat ttc ata gac tgg ggc caa ggg aca cta gt			415
Asp Phe Ile Asp Trp Gly Gln Gly Thr Leu			
130	135		
<210> 2			
<211> 437			
<212> DNA			
<213> Mus musculus			
<220>			
<221> CDS			
<222> (3)..(437)			
<400> 2			
aa gct tta cag tta ctc agc aca cag gac ctc acc atg agg ttc tct			47
Ala Leu Gln Leu Leu Ser Thr Gln Asp Leu Thr Met Arg Phe Ser			
1	5	10	15
ggt cag ttt ctg ggg gtg ctt atg ttc tgg atc tct gga gtc agt ggg			95
Val Gln Phe Leu Gly Val Leu Met Phe Trp Ile Ser Gly Val Ser Gly			
20	25	30	
gat att gtg ata acc cag gat gaa ctc tcc aat cct gtc act tct gga			143
Asp Ile Val Ile Thr Gln Asp Glu Leu Ser Asn Pro Val Thr Ser Gly			
35	40	45	
gaa tca gtt tcc atc tcc tgc agg tct agt aag agt ctc ctg tat aag			191
Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys			
50	55	60	
gat ggg aag aca tac ttg aat tgg ttt ctg cag aga cca gga caa tct			239
Asp Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg Pro Gly Gln Ser			
65	70	75	
cct cag ctc ctg atg tat ttg atg tcc acc cgt gca tca gga gtc tca			287
Pro Gln Leu Leu Met Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Ser			
80	85	90	95
gac cgg ttt agt ggc agt ggg tca ggc aca gat ttc acc ctg gaa atc			335
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile			
100	105	110	
agt aga gtg aag gct gag gat gtg ggt gtg tat tac tgt caa caa ctt			383
Ser Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu			
115	120	125	
gta gag tat cca ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aaa			431
Val Glu Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys			
130	135	140	
cgt acg			437
Arg Thr			
145			
<210> 3			
<211> 16			
<212> PRT			
<213> Mus musculus			

<400> 3
Arg Ser Ser Lys Ser Leu Leu Tyr Lys Asp Gly Lys Thr Tyr Leu Asn
1 5 10 15

<210> 4
<211> 48
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(48)

<400> 4
cgc tcg agt aag agt ctc ctg tat aag gat ggg aag aca tac ttg aat 48
Arg Ser Ser Lys Ser Leu Leu Tyr Lys Asp Gly Lys Thr Tyr Leu Asn
1 5 10 15

<210> 5
<211> 7
<212> PRT
<213> Mus musculus

<400> 5
Leu Met Ser Thr Arg Ala Ser
1 5

<210> 6
<211> 21
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(21)

<400> 6
ttg atg tcc acc cgg gca tca 21
Leu Met Ser Thr Arg Ala Ser
1 5

<210> 7
<211> 9
<212> PRT
<213> Mus musculus

<400> 7
Gln Gln Leu Val Glu Tyr Pro Phe Thr
1 5

<210> 8
<211> 27
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(27)

<400> 8
caa cag ctg gta gag tat cca ttc acg 27
Gln Gln Leu Val Glu Tyr Pro Phe Thr
1 5

<210> 9
<211> 5
<212> PRT
<213> Mus musculus

<400> 9
Gly Tyr Trp Met Ser
1 5

<210> 10
<211> 15
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(15)

<400> 10
ggc tac tgg atg tcc 15
Gly Tyr Trp Met Ser
1 5

<210> 11
<211> 19
<212> PRT
<213> Mus musculus

<400> 11
Glu Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser
1 5 10 15

Val Lys Gly

<210> 12
<211> 57
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(57)

<400> 12
gaa att aga ttg aaa tct gat aat tat gca aca cat tat gcg gag tct 48
Glu Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser
1 5 10 15

gtg aag ggg 57
Val Lys Gly

<210> 13

<400> 13
000

<210> 14
<400> 14
000

<210> 15
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
sequence

<400> 15
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser

<210> 16
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
sequence

<400> 16
Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
1 5 10 15

Ala Gln Ala

<210> 17
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Humanised
anti-CD23 antibody light chain variable region

<220>
<221> CDS
<222> (1)..(348)

<400> 17
gat att gtg atg act cag tct cca ctc tcc ctg ccc gtc acc cct gga 48
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

gag ccg gcc tcc atc tcc tgt cgc tcg agt aag agt ctc ctg tat aag 96
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys

20	25	30	
gat ggg aag aca tac ttg aat tgg tac ctg cag aag cca ggg cag tct			144
Asp Gly Lys Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser			
35	40	45	
cca cag ctc ctg atc tat ttg atg tcc acc cgg gca tca ggg gtc cct			192
Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Pro			
50	55	60	
gac agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc			240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile			
65	70	75	80
agc aga gtg gag gct gag gat gtt ggg gtt tat tac tgt caa cag ctg			288
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu			
85	90	95	
gta gag tat cca ttc acg ttc ggc caa ggg acc aag gtg gag atc aaa			336
Val Glu Tyr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys			
100	105	110	
cgt acg gtg gct			348
Arg Thr Val Ala			
115			
<210> 18			
<211> 1335			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Humanised			
anti-CD23 antibody heavy chain variable region.			
<220>			
<221> CDS			
<222> (1)..(1335)			
<400> 18			
gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta aag ccc ggg ggg			48
Glu Val Gln Leu Val Glu Ser Gly Gly Gln Leu Val Lys Pro Gly Gly			
1	5	10	15
tcc ctt aga ctc tcc tgt gca gct agc gga ttc act ttc agt ggc tac			96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr			
20	25	30	
tgg atg tcc tgg gtc cgc cag gct cca ggg aag ggg ctc gag tgg gtt			144
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val			
35	40	45	
gct gaa att aga ttg aaa tct gat aat tat gca aca cat tat gcg gag			192
Ala Glu Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu			
50	55	60	
tct gtg aag ggg aaa ttc acc atc tca aga gat gat tca aaa tct aga			240
Ser Val Lys Gly Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg			
65	70	75	80
ctg tat ctg caa atg aac agc ctg aaa acc gag gac aca gcc gtg tat			288

Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Thr	Glu	Asp	Thr	Ala	Val	Tyr	
				85					90					95		
tac	tgt	aca	gat	ttc	ata	gac	tgg	ggc	cag	gga	aca	cta	gtc	acc	gtc	336
Tyr	Cys	Thr	Asp	Phe	Ile	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	
			100					105					110			
tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	gca	ccc	tcc	384
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	
		115					120					125				
tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	ctg	gtc	aag	432
Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	
	130					135					140					
gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	ggc	gcc	ctg	480
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	
145					150				155						160	
acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	528
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	
				165					170					175		
tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	acc	576
Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	
			180					185					190			
cag	acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	agc	aac	acc	aag	gtg	624
Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	
		195					200					205				
gac	aag	aaa	gtg	gag	ccc	aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	672
Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	
	210					215					220					
ccg	tgc	cca	gca	cct	gaa	ctc	gcg	ggg	gca	ccg	tca	gtc	ttc	ctc	ttc	720
Pro	Cys	Pro	Ala	Pro	Glu	Leu	Ala	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	
225					230					235					240	
ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	768
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	
				245					250					255		
aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	816
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	
			260					265					270			
aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	864
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	
		275					280					285				
cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	912
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	
	290					295					300					
gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	960
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	
305					310					315					320	
tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	1008
Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	

	325	330	335	
aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg				1056
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg				
	340	345	350	
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc				1104
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly				
	355	360	365	
ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg				1152
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro				
	370	375	380	
gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc				1200
Glu Asn Asn Tyr Lys Thr Pro Pro Val Leu Asp Ser Asp Gly Ser				
	385	390	400	
ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag				1248
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln				
	405	410	415	
ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac				1296
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His				
	420	425	430	
tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga				1335
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys				
	435	440		

<210> 19
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo

<400> 19	
gatgaagctt tacagttact cagcacacag gacctcacca tggattttgg gctgatt	57

<210> 20
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo

<400> 20	
gatggactag tgtcccttgg cccca	25

<210> 21
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo

<400> 21
 gatgaagctt tacagttact cagcacacag gacctcacca tgaggttctc tggttcag 57

<210> 22
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo

<400> 22
 gatgcgtagc tytkatytcc avcttkgt 28

<210> 23
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo

<400> 23
 gatcaagctt ctctacagtt actgagcaca 30

<210> 24
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo

<400> 24
 aatcaagtat gtcttcccat ccttatacag gagactctta ctcgagcgcac aggagatgga 60
 ggc 63

<210> 25
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo

<400> 25
 cgctcgagta agagtctcct gtataaggat gggaagacat acttgaattg gtacctgcag 60
 aag 63

<210> 26
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo

<400> 26
 tgatgcccgg gtggacatca aatagatcag gagctg 36

<210> 27

<211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligo

 <400> 27
 ttgatgtcca cccgggcatc aggggtccct gacagg 36

 <210> 28
 <211> 84
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligo

 <400> 28
 agccacctga cgtttgatct ccaccttggc cccttggccg aacgtgaatg gatactctac 60
 cagctgttga cagtaataaa cccc 84

 <210> 29
 <211> 60
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligo

 <400> 29
 acacgaagct tcaccatggc ttgggtgtgg accttgctat tcctgatggc ggccgcccaa 60

 <210> 30
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligo

 <400> 30
 ctttaccaag cctccccag actccaccag ctgcacctct gcttgggcac tttgggcggc 60
 cgccat 66

 <210> 31
 <211> 60
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligo

 <400> 31
 ttggtaaagc ccgggggggc ccttagactc tcctgtgcag ctagcggatt cactttcagt 60

 <210> 32
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo

 <400> 32
 ccccttccct ggagcctggc ggacccagga catccagtag ccaactgaaag tgaatccgct 60

 <210> 33
 <211> 60
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligo

 <400> 33
 ggggaaggggc tcgagtgggt tgctgaaatt agattgaaat ctgataatta tgcaacacat 60

 <210> 34
 <211> 60
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligo

 <400> 34
 atcatctctt gagatgggtga atttcccctt cacagactcc gcataatgtg ttgcataatt 60

 <210> 35
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligo

 <400> 35
 atctcaagag atgattcaaa atctagactg tatctgcaaa tgaacagcct gaaaaccgag 60
 gacaca 66

 <210> 36
 <211> 69
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligo

 <400> 36
 ggtgactagt gttccctggc ccagctctat gaaatctgta cagtaataca cggctgtgtc 60
 ctcggtttt 69

 <210> 37
 <211> 48
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligo

 <400> 37

gctgctcctt ttaagctttg gggtaagga tcaactagta cagtctcc 48

<210> 38
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo

<400> 38
tgacggtgcc cccgcgagtt cagg 24

<210> 39
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo

<400> 39
cctgaactcg cgggggcacc gtca 24

<210> 40
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo

<400> 40
aagcttcggt cgaattcatt tacccggaga cag 33

<210> 41
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 41
actagtcgac atgaagtttc cttctcaact tctgctc 37

<210> 42
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
sequence

<400> 42
Thr Lys Leu Glu Ile Lys Arg Thr
1 5

<210> 43
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
sequence

<400> 43
Thr Lys Val Glu Ile Lys Arg Thr
1 5

<210> 44
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
sequence

<400> 44
Thr Lys Leu Glu Ile Arg Arg Thr
1 5

<210> 45
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
sequence

<400> 45
Thr Lys Val Glu Ile Arg Arg Thr
1 5

<210> 46
<211> 415
<212> DNA
<213> Mus musculus

<400> 46
actagtgtcc cttggcccca gtctatgaaa tctgtacagt aataaactcc actgtcttca 60
gctcttaagc tggtcatttg caggtagaga cgacttttgg aatcatctct tgagatgggtg 120
aacttccctt tcacagactc cgcataatgt gttgcataat taccagattt caatctaatt 180
tcagcaaccc actcaagccc cttctctgga gactggcgga cccaagacat ccagtagcca 240
ctgaaagtaa atccagaggc tacacaggag agtttcatgg atcctccagg ttgcaccaag 300
cctcctccag actcctcaag cttcacttca ctctggaccc cttttaaaag aacaataaaa 360
aaaatcagcc caaaatccat ggtgaggtcc tgtgtgctga gtaactgtaa agctt 415

<210> 47
<211> 437
<212> DNA
<213> Mus musculus

<400> 47

```
cgtacgtttt atttccaact ttgtccccga gccgaacgtg aatggatact ctacaagttg 60
ttgacagtaa tacacaccca catcctcagc cttcactcta ctgatttcca gggtgaaatc 120
tgtgcctgac ccaactgccac taaaccggtc tgagactcct gatgcacggg tggacatcaa 180
atacatcagg agctgaggag attgtcctgg tctctgcaga aaccaattca agtatgtcct 240
cccatcctta tacaggagac tcttactaga cctgcaggag atggaaactg attctccaga 300
agtgcacgga ttggagagtt catcctgggt tatcacaata tccccactga ctccagagat 360
ccagaacata agcaccacca gaaactgaac agagaacctc atgggtgaggt cctgtgtgct 420
gagtaactgt aaagctt 437
```

<210> 48

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanised
anti-CD23 antibody light chain variable region

<400> 48

```
agccaccgta cgtttgatct ccaccttggt cccttggcg aacgtgaatg gatactctac 60
cagctgttga cagtaataaa cccaacatc ctcagcctcc actctgctga ttttcagtgt 120
aaaatctgtg cctgatccac tgccactgaa cctgtcaggg acccctgatg cccgggtgga 180
catcaaatag atcaggagct gtggagactg ccctggcttc tgcaggatcc aattcaagta 240
tgtcttccca tccttatata ggagactctt actcgagcga caggagatgg aggccggctc 300
tccaggggtg acgggcaggg agagtggaga ctgagtcatc acaatatc 348
```

<210> 49

<211> 1335

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanised
anti-CD23 antibody heavy chain variable region

<400> 49

```
tcatttaccg ggagacaggg agaggctctt ctgctgttag tggttgtgca gagcctcatg 60
catcacggag catgagaaga cgttcccctg ctgccacctg ctcttgcca cggtagctt 120
gctgtagagg aagaaggagc cgtcggagtc cagcacggga ggctgtgtct tgtagtgtt 180
ctccggctgc ccattgctct ccaactccac ggcgatgtcg ctgggataga agcctttgac 240
caggcaggtc aggctgacct ggttcttggt cagctcatcc cgggatgggg gcagggtgta 300
cacctgtggt tctcggggct gccctttggc tttggagatg gttttctcga tgggggctgg 360
gagggtcttg ttggagacct tgcacttgta ctcccttgcca ttcagccagt cctggtgcag 420
gacgggtgagg acgctgacca cacggtagct gctgttgtag tgctcctccc gcggctttgt 480
cttggcatta tgcacctcca cgccgtccac gtaccagttg aacttgacct cagggtcttc 540
gtggctcagc tccaccacca cgcattgtgac ctcaggggtc cgggagatca tgagggtgtc 600
cttgggtttt ggggggaaga ggaagactga cggtgccccg gcgagttcag gtgctgggca 660
cggtgggcat gtgtgagttt tgtcacaaga tttgggctcc actttcttgt ccaccttggt 720
gttgctgggc ttgtgattca cgttgcatag gtaggctctg gtgccaagc tgctggaggg 780
cacggtcacc acgctgctga gggagttagt tcttaggac tgtaggacag ccgggaaggt 840
gtgcacgcgc ctggtcaggg cgcctgagtt ccacgacacc gtcacogggt cggggaagta 900
gtccttgacc aggcagccca gggccgctgt gccccagag gtgctcttgg aggagggtgc 960
cagggggaag accgatgggc ccttggtgga ggctgaggag acgggtgacta gtgttccctg 1020
gccccagtct atgaaatctg tacagtaata cacggctgtg tctcgggtt tcaggctgtt 1080
catttgacga tacagtctag attttgaatc atctcttag atgggtgaatt tccccttcac 1140
agactccgca taatgtgttg cataattatc agatttcaat ctaatttcag caaccactc 1200
gagccccctt cctggagcct ggcggaccca ggacatccag tagccactga aagtgaatcc 1260
gctagctgca caggagagtc taagggaccc cccgggcttt accaagcctc ccccagactc 1320
caccagctgc acctc 1335
```

<210> 50
<211> 137
<212> PRT
<213> Mus musculus

<400> 50
Ala Leu Gln Leu Leu Ser Thr Gln Asp Leu Thr Met Asp Phe Gly Leu
1 5 10 15
Ile Phe Phe Ile Val Leu Leu Lys Gly Val Gln Ser Glu Val Lys Leu
20 25 30
Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu
35 40 45
Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Gly Tyr Trp Met Ser Trp
50 55 60
Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg
65 70 75 80
Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser Val Lys Gly
85 90 95
Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg Leu Tyr Leu Gln
100 105 110
Met Asn Ser Leu Arg Ala Glu Asp Ser Gly Val Tyr Tyr Cys Thr Asp
115 120 125
Phe Ile Asp Trp Gly Gln Gly Thr Leu
130 135

<210> 51
<211> 145
<212> PRT
<213> Mus musculus

<400> 51
Ala Leu Gln Leu Leu Ser Thr Gln Asp Leu Thr Met Arg Phe Ser Val
1 5 10 15
Gln Phe Leu Gly Val Leu Met Phe Trp Ile Ser Gly Val Ser Gly Asp
20 25 30
Ile Val Ile Thr Gln Asp Glu Leu Ser Asn Pro Val Thr Ser Gly Glu
35 40 45
Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys Asp
50 55 60
Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro
65 70 75 80
Gln Leu Leu Met Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Ser Asp
85 90 95
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile Ser
100 105 110
Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu Val

115 120 125
 Glu Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
 130 135 140

Thr
 145

<210> 52
 <211> 116
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: Humanised
 anti-CD23 antibody light chain variable region

<400> 52
 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys
 20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Pro
 50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
 85 90 95

Val Glu Tyr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

Arg Thr Val Ala
 115

<210> 53
 <211> 444
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: Humanised
 anti-CD23 antibody heavy chain variable region.

<400> 53
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
 20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Glu Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu
 50 55 60

Ser Val Lys Gly Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg

65	70					75					80				
Leu Tyr Leu Gln Met	Asn Ser Leu Lys Thr	Glu Asp Thr Ala Val Tyr	85			90			95						
Tyr Cys Thr Asp Phe Ile Asp Trp Gly Gln Gly Thr Leu Val Thr Val			100			105			110						
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser			115			120			125						
Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys			130			135			140						
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu				150			155							160	
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu				165			170							175	
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr			180				185						190		
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val			195			200			205						
Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro			210			215			220						
Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser Val Phe Leu Phe				230			235							240	
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val				245			250							255	
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe				260			265							270	
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro			275			280			285						
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr			290			295			300						
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val			305			310			315					320	
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala				325			330							335	
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg			340				345						350		
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly			355			360			365						
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro			370			375			380						
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser			385			390			395					400	

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440
